RAW SEQUENCE LISTING   DATE: 09/12/2005
PATENT APPLICATION: US/08/989,896   TIME: 12:57:56

Input Set: N:\Crf3\RULE60\08989896.raw.txt
Output Set: N:\CRF4\09092005\H989896.raw

SEQUENCE LISTING

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 3  (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Gehrmann, Mathias
 6                     Seemann, Gerhard
 7                     Bosslet, Klaus
 8                     Czech, Joerg
10      (ii) TITLE OF INVENTION: Fusion Protein for Prodrug Activity
12      (iii) NUMBER OF SEQUENCES: 18
14      (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
16                         Dunner
17          (B) STREET: 1300 I Street, N.W.
18          (C) CITY: Washington
19          (D) STATE: D.C.
20          (E) COUNTRY: USA
21          (F) ZIP: 20005-3315
23      (v) COMPUTER READABLE FORM:
24          (A) MEDIUM TYPE: Floppy disk
25          (B) COMPUTER: IBM PC compatible
26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29      (vi) CURRENT APPLICATION DATA:
C--> 30      (A) APPLICATION NUMBER: US/08/989,896
C--> 31      (B) FILING DATE: 12-Dec-1997
33      (vii) PRIOR APPLICATION DATA:
W--> 34      (A) APPLICATION NUMBER: US/08/475,826
35           (B) FILING DATE: 07-JUN-1995
W--> 36      (A) APPLICATION NUMBER: US 08/129,379
37           (B) FILING DATE: 30-SEP-1993
W--> 39      (A) APPLICATION NUMBER: DE P 42 33 152.8
40           (B) FILING DATE: 02-OCT-1992
42      (viii) ATTORNEY/AGENT INFORMATION:
43          (A) NAME: Barker, M. P.
44          (B) REGISTRATION NUMBER: 32,013
45          (C) REFERENCE/DOCKET NUMBER: 02481.1337-00000
47      (ix) TELECOMMUNICATION INFORMATION:
48          (A) TELEPHONE: 202-408-4000
49          (B) TELEFAX: 202-408-4400
52  (2) INFORMATION FOR SEQ ID NO: 1:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 3314 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: single
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Input Set : N:\CRF3\RULE60\08989896.raw.txt
Output Set: N:\CRF4\09092005\H989896.raw

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 58            (D) TOPOLOGY: linear
 60      (ii) MOLECULE TYPE: DNA (genomic)
 63      (ix) FEATURE:
 64            (A) NAME/KEY: sig_peptide
 65            (B) LOCATION: 145..283
 67      (ix) FEATURE:
 68            (A) NAME/KEY: mat_peptide
 69            (B) LOCATION: join(284..1003, 1069..1119, 1263..3161)
 71      (ix) FEATURE:
 72            (A) NAME/KEY: CDS
 73            (B) LOCATION: join(145..189, 272..1003, 1069..1119, 1263..3161)
 76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

 78 CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA ATCTACATGG      60
 80 TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA GATCACAGTT CTCTCTACAG     120
 82 TTACTGAGCA CACAGGACCT CACC ATG GGA TGG AGC TGT ATC ATC CTC TTC        171
 83                           Met Gly Trp Ser Cys Ile Ile Leu Phe
 84                           -19                 -15
 86 TTG GTA GCA ACA GCT ACA GGTAAGGGGC TCACAGTAGC AGGCTTGAGG             219
 87 Leu Val Ala Thr Ala Thr
 88 -10                 -5
 90 TCTGGACATA TATATGGGTG ACAATGACAT CCACTTTGCC TTTCTCTCCA CA GGT        274
 91                                                             Gly
 92                                                             -4
 94 GTC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA      322
 95 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 96           1               5                   10
 98 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC ACC ATC      370
 99 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile
100        15                  20                  25
102 AGC AGT GGT TAT AGC TGG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT      418
103 Ser Ser Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly
104 30                  35                  40                  45
106 CTT GAG TGG ATT GGA TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC      466
107 Leu Glu Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn
108                 50                  55                  60
110 CCC TCT CTC AAA AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC      514
111 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
112            65                  70                  75
114 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC      562
115 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
116         80                  85                  90
118 TAT TAT TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC      610
119 Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val
120        95                  100                 105
122 TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG      658
123 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
124 110                 115                 120                 125
126 GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC CAG      706
127 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln
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128                 130                135                140
130 AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC     754
131 Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
132          145                150                155
134 TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC CAG CAG AAG     802
135 Cys Ser Thr Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys
136          160                165                170
138 CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA TCC AAC CTG GCT     850
139 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala
140      175                180                185
142 TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC     898
143 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
144 190                195                200                205
146 ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC     946
147 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
148                210                215                220
150 TGC CAT CAG TGG AGT AGT TAT CCC ACG TTC GGC CAA GGG ACC AAG CTG     994
151 Cys His Gln Trp Ser Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Leu
152                225                230                235
154 GAG ATC AAA GGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTGGATCTG            1043
155 Glu Ile Lys
156          240
158 AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA ACC CCA CTT GGT GAC ACA     1095
159                            Glu Leu Lys Thr Pro Leu Gly Asp Thr
160                                            245
162 ACT CAC ACA TGC CCA CGG TGC CCA GGTAAGCCAG CCCAGGACTC GCCCTCCAGC    1149
163 Thr His Thr Cys Pro Arg Cys Pro
164 250                255
166 TCAAGGCGGG ACAAGAGCCC TAGAGTGGCC TGAGTCCAGG GACAGGCCCC AGCAGGGTGC   1209
168 TGACGCATCC ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG      1265
169                                                              Ala
172 GCG GCG GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG     1313
173 Ala Ala Ala Val Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser
174      260                265                270
176 CGG GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC     1361
177 Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe
178 275                280                285                290
180 TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG CCG     1409
181 Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro
182                295                300                305
184 CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC AGC TTC     1457
185 Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe
186                310                315                320
188 AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC GGC TGG GTG     1505
189 Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val
190          325                330                335
192 TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG ACC CAG GAC CTG     1553
193 Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu
194          340                345                350
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196 CGC ACA AGA GTC GTG CTG AGG ATT GGC AGT GCC CAT TCC TAT GCC ATC     1601
197 Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile
198 355             360                 365                 370
200 GTG TGG GTG AAT GGG GTC GAC ACG CTA GAG CAT GAG GGG GGC TAC CTC     1649
201 Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu
202             375                 380                 385
204 CCC TTC GAG GCC GAC ATC AGC AAC CTG GTC CAG GTG GGG CCC CTG CCC     1697
205 Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro
206             390                 395                 400
208 TCC CGG CTC CGA ATC ACT ATC GCC ATC AAC AAC ACA CTC ACC CCC ACC     1745
209 Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr
210             405                 410                 415
212 ACC CTG CCA CCA GGG ACC ATC CAA TAC CTG ACT GAC ACC TCC AAG TAT     1793
213 Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr
214     420                 425—                430
216 CCC AAG GGT TAC TTT GTC CAG AAC ACA TAT TTT GAC TTT TTC AAC TAC     1841
217 Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr
218 435                 440                 445                 450
220 GCT GGA CTG CAG CGG TCT GTA CTT CTG TAC ACG ACA CCC ACC ACC TAC     1889
221 Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr
222             455                 460                 465
224 ATC GAT GAC ATC ACC GTC ACC ACC AGC GTG GAG CAA GAC AGT GGG CTG     1937
225 Ile Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu
226             470                 475                 480
228 GTG AAT TAC CAG ATC TCT GTC AAG GGC AGT AAC CTG TTC AAG TTG GAA     1985
229 Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu
230             485                 490                 495
232 GTG CGT CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG     2033
233 Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly
234     500                 505                 510
236 ACC CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC     2081
237 Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr
238 515                 520                 525                 530
240 CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG CTG     2129
241 Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu
242             535                 540                 545
244 ACT GCA CAG ACG TCA CTG GGG CCT GTG TCT GAC TTC TAC ACA CTC CCT     2177
245 Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro
246             550                 555                 560
248 GTG GGG ATC CGC ACT GTG GCT GTC ACC AAG AGC CAG TTC CTC ATC AAT     2225
249 Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn
250             565                 570                 575
252 GGG AAA CCT TTC TAT TTC CAC GGT GTC AAC AAG CAT GAG GAT GCG GAC     2273
253 Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp
254     580                 585                 590
256 ATC CGA GGG AAG GGC TTC GAC TGG CCG CTG CTG GTG AAG GAC TTC AAC     2321
257 Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn
258 595                 600                 605                 610
260 CTG CTT CGC TGG CTT GGT GCC AAC GCT TTC CGT ACC AGC CAC TAC CCC     2369
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261 Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro
262               615                     620                 625
264 TAT GCA GAG GAA GTG ATG CAG ATG TGT GAC CGC TAT GGG ATT GTG GTC    2417
265 Tyr Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val
266           630                     635                 640
268 ATC GAT GAG TGT CCC GGC GTG GGC CTG GCG CTG CCG CAG TTC TTC AAC    2465
269 Ile Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn
270           645                     650                 655
272 AAC GTT TCT CTG CAT CAC CAC ATG CAG GTG ATG GAA GAA GTG GTG CGT    2513
273 Asn Val Ser Leu His His His Met Gln Val Met Glu Glu Val Val Arg
274     660                     665                 670
276 AGG GAC AAG AAC CAC CCC GCG GTC GTG ATG TGG TCT GTG GCC AAC GAG    2561
277 Arg Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu
278 675                     680                 685                 690
280 CCT GCG TCC CAC CTA GAA TCT GCT GGC TAC TAC TTG AAG ATG GTG ATC    2609
281 Pro Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile
282                     695                 700                 705
284 GCT CAC ACC AAA TCC TTG GAC CCC TCC CGG CCT GTG ACC TTT GTG AGC    2657
285 Ala His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser
286               710                 715                 720
288 AAC TCT AAC TAT GCA GCA GAC AAG GGG GCT CCG TAT GTG GAT GTG ATC    2705
289 Asn Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile
290           725                     730                 735
292 TGT TTG AAC AGC TAC TAC TCT TGG TAT CAC GAC TAC GGG CAC CTG GAG    2753
293 Cys Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu
294     740                     745                 750
296 TTG ATT CAG CTG CAG CTG GCC ACC CAG TTT GAG AAC TGG TAT AAG AAG    2801
297 Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys
298 755                     760                 765                 770
300 TAT CAG AAG CCC ATT ATT CAG AGC GAG TAT GGA GCA GAA ACG ATT GCA    2849
301 Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala
302                     775                 780                 785
304 GGG TTT CAC CAG GAT CCA CCT CTG ATG TTC ACT GAA GAG TAC CAG AAA    2897
305 Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys
306               790                 795                 800
308 AGT CTG CTA GAG CAG TAC CAT CTG GGT CTG GAT CAA AAA CGC AGA AAA    2945
309 Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys
310           805                     810                 815
312 TAT GTG GTT GGA GAG CTC ATT TGG AAT TTT GCC GAT TTC ATG ACT GAA    2993
313 Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu
314     820                     825                 830
316 CAG TCA CCG ACG AGA GTG CTG GGG ATT AAA AAG GGG ATC TTC ACT CGG    3041
317 Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg
318 835                     840                 845                 850
320 CAG AGA CAA CCA AAA AGT GCA GCG TTC CTT TTG CGA GAG AGA TAC TGG    3089
321 Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp
322                     855                 860                 865
324 AAG ATT GCC AAT GAA ACC AGG TAT CCC CAC TCA GTA GCC AAG TCA CAA    3137
325 Lys Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala Lys Ser Gln
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VERIFICATION SUMMARY   DATE: 09/12/2005
PATENT APPLICATION... US/08/989,896   TIME: 12:57:57

Input Set : N:\Crf3\RULE60\08989896.raw.txt
Output Set: N:\CRF4\09092005\H989896.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:39 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)

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